

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,106

DATE: 07/06/2001

TIME: 12:20:49

Input Set : A:\cpg.txt

Output Set: N:\CRF3\07062001\I873106.raw

4 <110> APPLICANT: Reinherz, Ellis L.
 5 Freund, Christian
 6 Li, Jing
 7 Nishizawa, Kazuhisa
 8 Wagner, Gerhard
 10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2
 11 Binding Protein (CD2BP2)
 14 <130> FILE REFERENCE: 1062.1021-004
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/873,106
 C--> 16 <141> CURRENT FILING DATE: 2001-06-01
 16 <150> PRIOR APPLICATION NUMBER: US 60/111,007
 17 <151> PRIOR FILING DATE: 1998-12-04
 19 <150> PRIOR APPLICATION NUMBER: US 60/115,647
 20 <151> PRIOR FILING DATE: 1999-01-13
 22 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993
 23 <151> PRIOR FILING DATE: 1999-11-15
 25 <160> NUMBER OF SEQ ID NOS: 25
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1299
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (121)...(1143)
 38 <400> SEQUENCE: 1
 39 agtcctcttc cgggtgatgg cggcgggtgc cccggatgta gccctggcgc aagcatctct 60
 40 tcttttttcc acctgcctt ccgcggattc ccagcttgag aaacacctct ttgccccgtc 120
 41 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
 42 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
 43 1 5 10 15
 45 gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
 46 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
 47 20 25 30
 49 ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
 50 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
 51 35 40 45
 53 agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312
 54 Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
 55 50 55 60
 57 atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360
 58 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
 59 65 70 75 80
 61 agc gag ggg ggt ggt cgg atc aca ccc ttt aac ctg cag gag gag atg 408
 62 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
 63 85 90 95
 65 gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat 456

Does Not Comply
 Corrected Diskette Needed

See p.5

After an initial
 correction of
 format errors,
 (second copy
 attached) the
 sequence listing
 was found to still
 be errored.

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66	Glu	Glu	Gly	His	Phe	Asp	Ala	Asp	Gly	Asn	Tyr	Phe	Leu	Asn	Arg	Asp	
67				100					105					110			
69	gct	cag	atc	cga	gac	agc	tgg	ctg	gac	aac	att	gac	tgg	gtg	aag	atc	504
70	Ala	Gln	Ile	Arg	Asp	Ser	Trp	Leu	Asp	Asn	Ile	Asp	Trp	Val	Lys	Ile	
71			115					120					125				
73	cgg	gag	cgg	cca	cct	ggc	cag	cgc	cag	gcc	tca	gac	tcg	gag	gag	gag	552
74	Arg	Glu	Arg	Pro	Pro	Gly	Gln	Arg	Gln	Ala	Ser	Asp	Ser	Glu	Glu	Glu	
75		130						135				140					
77	gac	agc	ttg	ggc	cag	acc	tca	atg	agt	gcc	caa	gcc	ctc	ttg	gag	gga	600
78	Asp	Ser	Leu	Gly	Gln	Thr	Ser	Met	Ser	Ala	Gln	Ala	Leu	Leu	Glu	Gly	
79	145				150					155					160		
81	ctt	ttg	gag	ctc	cta	ttg	cct	aga	gag	aca	gtg	gct	ggg	gca	ctg	agg	648
82	Leu	Leu	Glu	Leu	Leu	Leu	Pro	Arg	Glu	Thr	Val	Ala	Gly	Ala	Leu	Arg	
83				165					170				175				
85	cgt	ctg	ggg	gcc	cga	gga	gga	ggc	aaa	ggg	aga	aag	ggg	cct	ggg	caa	696
86	Arg	Leu	Gly	Ala	Arg	Gly	Gly	Gly	Lys	Gly	Arg	Lys	Gly	Pro	Gly	Gln	
87			180					185					190				
89	ccc	agt	tcc	cct	cag	cgc	ctg	gac	cgg	ctc	tcc	ggg	ttg	gcc	gac	cag	744
90	Pro	Ser	Ser	Pro	Gln	Arg	Leu	Asp	Arg	Leu	Ser	Gly	Leu	Ala	Asp	Gln	
91		195						200				205					
93	atg	gtg	gcc	cgg	ggc	aac	ctt	ggt	gtg	tac	cag	gaa	aca	agg	gaa	cgg	792
94	Met	Val	Ala	Arg	Gly	Asn	Leu	Gly	Val	Tyr	Gln	Glu	Thr	Arg	Glu	Arg	
95		210				215					220						
97	ttg	gct	atg	cgt	ctg	aag	ggt	ttg	ggg	tgt	cag	acc	cta	gga	ccc	cac	840
98	Leu	Ala	Met	Arg	Leu	Lys	Gly	Leu	Gly	Cys	Gln	Thr	Leu	Gly	Pro	His	
99	225			230				235				240					
101	aat	ccc	aca	ccc	cca	ccc	tcc	ctg	gac	atg	ttc	gct	gag	gag	ttg	gcg	888
102	Asn	Pro	Thr	Pro	Pro	Pro	Ser	Leu	Asp	Met	Phe	Ala	Glu	Glu	Leu	Ala	
103				245				250					255				
105	gag	gag	gaa	ctg	gag	acc	cca	acc	cct	acc	cag	aga	gga	gaa	gca	gag	936
106	Glu	Glu	Glu	Leu	Glu	Thr	Pro	Thr	Pro	Thr	Gln	Arg	Gly	Glu	Ala	Glu	
107			260					265					270				
109	tcg	cgg	gga	gat	ggt	ctg	gtg	gat	gtg	atg	tgg	gaa	tat	aag	tgg	gag	984
110	Ser	Arg	Gly	Asp	Gly	Leu	Val	Asp	Val	Met	Trp	Glu	Tyr	Lys	Trp	Glu	
111		275				280					285						
113	aac	acg	ggg	gat	gcc	gag	ctg	tat	ggg	ccc	ttc	acc	agc	gcc	cag	atg	1032
114	Asn	Thr	Gly	Asp	Ala	Glu	Leu	Tyr	Gly	Pro	Phe	Thr	Ser	Ala	Gln	Met	
115		290				295					300						
117	cag	acc	tgg	gtg	agt	gaa	ggc	tac	ttc	ccg	gac	ggt	ggt	tat	tgc	cgg	1080
118	Gln	Thr	Trp	Val	Ser	Glu	Gly	Tyr	Phe	Pro	Asp	Gly	Val	Tyr	Cys	Arg	
119	305				310				315				320				
121	aag	ctg	gac	ccc	cct	ggt	ggt	cag	ttc	tac	aac	tcc	aaa	cgc	att	gac	1128
122	Lys	Leu	Asp	Pro	Pro	Gly	Gly	Gln	Phe	Tyr	Asn	Ser	Lys	Arg	Ile	Asp	
123				325				330				335					
125	ttt	gac	ctc	tac	acc	tgagcctgct	gggggcccag	tttgggtgggc	ccttctttcc								1183
126	Phe	Asp	Leu	Tyr	Thr												
127			340														
129	tgga	ctttgt	ggaggaggca	ccaagtgtct	caggcagcga	ggaaattgga	ggccattttt										1243
130	cag	tcaattt	ccctttccca	ataaaagcct	tagttgtgta	aaaaaaaaa	aaaaaa										1299

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Input Set : A:\cpg.txt

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132 <210> SEQ ID NO: 2
133 <211> LENGTH: 341
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 2
138 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
139 1 5 10 15
140 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
141 20 25 30
142 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
143 35 40 45
144 Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
145 50 55 60
146 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
147 65 70 75 80
148 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
149 85 90 95
150 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
151 100 105 110
152 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
153 115 120 125
154 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
155 130 135 140
156 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
157 145 150 155 160
158 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
159 165 170 175
160 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
161 180 185 190
162 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
163 195 200 205
164 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
165 210 215 220
166 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
167 225 230 235 240
168 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
169 245 250 255
170 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
171 260 265 270
172 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
173 275 280 285
174 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
175 290 295 300
176 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
177 305 310 315 320
178 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
179 325 330 335
180 Phe Asp Leu Tyr Thr
181 340

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Input Set : A:\cpg.txt
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184 <210> SEQ ID NO: 3
185 <211> LENGTH: 26
186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 3
190 Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr
191 1 5 10 15
192 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly
193 20 25
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 27
198 <212> TYPE: PRT
199 <213> ORGANISM: Caenorhabditis elegans
201 <400> SEQUENCE: 4
202 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu
203 1 5 10 15
204 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly
205 20 25
208 <210> SEQ ID NO: 5
209 <211> LENGTH: 27
210 <212> TYPE: PRT
211 <213> ORGANISM: Caenorhabditis elegans
213 <400> SEQUENCE: 5
214 Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn
215 1 5 10 15
216 Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu
217 20 25
220 <210> SEQ ID NO: 6
221 <211> LENGTH: 27
222 <212> TYPE: PRT
223 <213> ORGANISM: Caenorhabditis elegans
225 <400> SEQUENCE: 6
226 Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu
227 1 5 10 15
228 Asp Trp Tyr Gln Lys Gly Tyr Phe Ser Asp Asn
229 20 25
232 <210> SEQ ID NO: 7
233 <211> LENGTH: 29
234 <212> TYPE: PRT
235 <213> ORGANISM: Saccharomyces cerevisiae
237 <400> SEQUENCE: 7
238 Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
239 1 5 10 15
240 Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr
241 20 25
244 <210> SEQ ID NO: 8
245 <211> LENGTH: 27
246 <212> TYPE: PRT
247 <213> ORGANISM: Saccharomyces cerevisiae

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249 <400> SEQUENCE: 8

250 Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser

251 1 5 10 15

252 Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr

253 20 25

256 <210> SEQ ID NO: 9

257 <211> LENGTH: 17

258 <212> TYPE: PRT

259 <213> ORGANISM: Artificial Sequence

261 <220> FEATURE:

262 <223> OTHER INFORMATION: Motif in CD2 binding region of CD2BP2

265 <221> NAME/KEY: VARIANT

266 <222> LOCATION: (1)...(2)

267 <223> OTHER INFORMATION: Xaa = Any Amino Acid

269 <221> NAME/KEY: VARIANT

270 <222> LOCATION: (3)...(3)

271 <223> OTHER INFORMATION: Xaa can be Tyr or Phe

273 <221> NAME/KEY: VARIANT

274 <222> LOCATION: (4)...(7)

275 <223> OTHER INFORMATION: Xaa = Any Amino Acid

277 <221> NAME/KEY: VARIANT

278 <222> LOCATION: (8)...(8)

279 <223> OTHER INFORMATION: Xaa can be Met or Val

281 <221> NAME/KEY: VARIANT

282 <222> LOCATION: (9)...(15)

283 <223> OTHER INFORMATION: Xaa = Any Amino Acid

285 <400> SEQUENCE: 9

W--> 286 Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Thr

287 1 5 10 15

288 Phe

292 <210> SEQ ID NO: 10

293 <211> LENGTH: 6

294 <212> TYPE: PRT

295 <213> ORGANISM: Artificial Sequence

297 <220> FEATURE:

298 <223> OTHER INFORMATION: CD2BP2 binding region

301 <400> SEQUENCE: 10

302 Pro Pro Pro Gly His Arg

303 1 5

306 <210> SEQ ID NO: 11

307 <211> LENGTH: 70

308 <212> TYPE: PRT

309 <213> ORGANISM: Homo sapiens

311 <400> SEQUENCE: 11

312 Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro

313 1 5 10 15

314 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro

315 20 25 30

316 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro

Position 1...2 are
not Xaa's.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/873,106

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Input Set : A:\cpg.txt

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9